SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Zancope-Oliveia, Rosely M.
                et al.,

(ii) TITLE OF INVENTION: Nucleic Acids of the M Antigen
         Gene of Histoplasma Capsulatum, Isolated and
Recombinantly-Produced
         Antigens, Vaccines and Antibodies, Method

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:
    (A) ADDRESSEE: Fitch, Even, Tabin & Flannery
    (B) STREET: 135 South LaSalle Street, Suite 900
    (C) CITY: Chicago
    (D) STATE: IL
    (E) COUNTRY: USA
    (F) ZIP: 60603-4277

(v) COMPUTER READABLE FORM:
    (A) MEDIUM TYPE: Diskette
    (B) COMPUTER: IBM Compatible
    (C) OPERATING SYSTEM: Windows
    (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
    (A) APPLICATION NUMBER:
    (B) FILING DATE:
    (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER:
    (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
    (A) NAME: Kaba, Richard A
    (B) REGISTRATION NUMBER: 30,562
    (C) REFERENCE/DOCKET NUMBER: 6314/62527

(ix) TELECOMMUNICATION INFORMATION:
    (A) TELEPHONE: 312-372-7842
    (B) TELEFAX: 312-372-7848
    (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 3862 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Histoplasma capsulatum
    (B) STRAIN: var. capsulatum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TTGGTCCCTA CCCTCTCCAA CACTATCTGC ATATGTAATA TATATCGATA TCTAACTGCC    420
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TCACATCCTA TAATAACTGG TCGAATATCA CAGCCGCATC CTTCTTGAAC GCGGCAGGAA    960
AGCAGACACC AGTATTCGTG CGGTTTTCTA CAGTCGCTGG TAGCAGAGGC AGTGTTGACT   1020
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TGTTTCTCTG CTCTGTCGGT TGCTCTTTTC GTCTTTTTCT ATATCTTCAA CTAAGACTGA   1680
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CAAGTTTGAT TTCGATCTAT TAGATCCCAC CAAAATCATC CCAGAAGAAC TTGTTCCTTT   1800
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GAAGCGTATA TCTAAATATA TTTCCACAGT TCCAACCAGG TCATGTAGTT CGCGGAATCG   1980
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TGACTATCTG ATAAAAATGT CTGTATTTCC GCTTCACGAC GCATGTTATG ACTTTCGAAT   3720
ATAGATAAAA CCTGAACGAT TTAGCCCCTG TTGGGGGAAA TAGGGGTTAG GGGGGCGAGC   3780
TACATATCAT TCCCATATGA CCAAAAACTA AAATAGATAT ATATATATAT ATATATATAT   3840
ACAACACCTT CAAAAAGGAT CC                                           3862
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                (2) INFORMATION FOR SEQ ID NO:2:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 707 amino acids
                (B) TYPE: amino acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
            (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Pro Ser Gly Gln Lys Gly Pro Leu Asp Arg Arg His Asp Thr Leu
1               5                   10                  15
Ser Asp Pro Thr Asp Gln Phe Leu Ser Lys Phe Tyr Ile Asp Asp Glu
            20                  25                  30
Gln Ser Val Leu Thr Thr Asp Val Gly Gly Pro Ile Glu Asp Gln His
        35                  40                  45
Ser Leu Lys Ala Gly Asn Arg Gly Pro Thr Leu Leu Glu Asp Phe Ile
    50                  55                  60
Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg Val Pro Glu Arg
65                  70                  75                  80
Ala Val His Ala Arg Gly Ala Gly Ala His Gly Val Phe Thr Ser Tyr
                85                  90                  95
Asn Asn Trp Ser Asn Ile Thr Ala Ala Ser Phe Leu Asn Ala Ala Gly
            100                 105                 110
Lys Gln Thr Pro Val Phe Val Arg Phe Ser Thr Val Ala Gly Ser Arg
        115                 120                 125
Gly Ser Val Asp Ser Ala Arg Asp Ile His Gly Phe Ala Thr Arg Leu
    130                 135                 140
Tyr Thr Asp Glu Gly Asn Phe Asp Ile Val Gly Asn Asn Val Pro Val
145                 150                 155                 160
Phe Phe Ile Gln Asp Ala Ile Gln Phe Pro Asp Leu Ile His Ala Val
                165                 170                 175
Lys Pro Gln Pro Asp Ser Glu Ile Pro Gln Ala Ala Thr Ala His Asp
        180                 185                 190
Thr Ala Trp Asp Phe Leu Ser Gln Gln Pro Ser Ser Leu His Ala Leu
    195                 200                 205
Phe Trp Ala Met Ser Gly His Gly Ile Pro Arg Ser Met Arg His Val
210                 215                 220
Asp Gly Trp Gly Val His Thr Phe Arg Leu Val Thr Asp Glu Gly Asn
225                 230                 235                 240
Ser Thr Leu Val Lys Phe Arg Trp Lys Thr Leu Gln Gly Arg Ala Gly
                245                 250                 255
Leu Val Trp Glu Glu Ala Gln Ala Leu Gly Gly Lys Asn Pro Asp Phe
    260                 265                 270
His Arg Gln Asp Leu Trp Asp Ala Ile Glu Ser Gly Arg Tyr Pro Glu
    275                 280                 285
Trp Glu Leu Gly Phe Gln Leu Val Asn Glu Ala Asp Gln Ser Lys Phe
    290                 295                 300
Asp Phe Asp Leu Leu Asp Pro Thr Lys Ile Ile Pro Glu Glu Leu Val
305                 310                 315                 320
Pro Phe Thr Pro Ile Gly Lys Met Val Leu Asn Arg Asn Pro Lys Ser
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Gln Leu Pro Ile Asn Arg Pro Arg Ile Pro Phe His Asn Asn Asn Arg
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            420                 425                 430
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    435                 440                 445
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    450                 455                 460
Leu Phe Tyr Asn Ser Leu Thr Val Phe Glu Lys Gln Phe Leu Val Asn
465                 470                 475                 480
Ala Met Arg Phe Glu Asn Ser His Val Arg Ser Glu Thr Val Arg Lys
            485                 490                 495
Asn Val Ile Ile Gln Leu Asn Arg Val Asp Asn Asp Leu Ala Arg Arg
            500                 505                 510
Val Ala Leu Ala Ile Gly Val Glu Pro Pro Ser Pro Asp Pro Thr Phe
    515                 520                 525
Tyr His Asn Lys Ala Thr Val Pro Ile Gly Thr Phe Gly Thr Asn Leu
    530                 535                 540
Leu Arg Leu Asp Gly Leu Lys Ile Ala Leu Leu Thr Arg Asp Asp Gly
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Ser Phe Thr Ile Ala Glu Gln Leu Arg Ala Ala Phe Asn Ser Ala Asn
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                580                  585                  590
Gly Val Asn Met Thr Tyr Ser Gly Ala Asp Gly Ser Ile Phe Asp Ala
            595                  600                  605
Val Ile Val Val Gly Gly Leu Leu Thr Ser Ala Ser Thr Gln Tyr Pro
        610                  615                  620
Arg Gly Arg Pro Leu Arg Ile Ile Thr Asp Ala Tyr Ala Tyr Gly Lys
625                  630                  635                  640
Pro Val Gly Ala Val Gly Asp Gly Ser Asn Glu Ala Leu Arg Asp Val
                645                  650                  655
Leu Met Ala Ala Gly Gly Asp Ala Ser Asn Gly Leu Asp Gln Pro Gly
            660                  665                  670
Val Tyr Ile Ser Asn Asp Val Ser Glu Ala Tyr Val Arg Ser Val Leu
            675                  680                  685
Asp Gly Leu Thr Ala Tyr Arg Phe Leu Asn Arg Phe Pro Leu Asp Arg
    690                  695                  700 .
Ser Leu Val
705.
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(2) INFORMATION FOR SEQ ID NO:3:

　　(i) SEQUENCE CHARACTERISTICS:
　　　　(A) LENGTH: 8 amino acids
　　　　(B) TYPE: amino acid
　　　　(C) STRANDEDNESS: single
　　　　(D) TOPOLOGY: linear
　　(ii) MOLECULE TYPE: None

　　(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Ser Asp Pro Thr Asp Gln Phe Leu
1                   5
```

(2) INFORMATION FOR SEQ ID NO:4:

　　(i) SEQUENCE CHARACTERISTICS:
　　　　(A) LENGTH: 15 amino acids
　　　　(B) TYPE: amino acid
　　　　(C) STRANDEDNESS: single
　　　　(D) TOPOLOGY: linear
　　(ii) MOLECULE TYPE: None

　　(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Asp Phe Ile Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg
1               5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO:5:

　　(i) SEQUENCE CHARACTERISTICS:
　　　　(A) LENGTH: 9 amino acids
　　　　(B) TYPE: amino acid
　　　　(C) STRANDEDNESS: single
　　　　(D) TOPOLOGY: linear
　　(ii) MOLECULE TYPE: None

　　(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Thr Leu Gln Gly Arg Ala Gly Leu Val
1               5
```

(2) INFORMATION FOR SEQ ID NO:6:

　　(i) SEQUENCE CHARACTERISTICS:
　　　　(A) LENGTH: 16 amino acids
　　　　(B) TYPE: amino acid
　　　　(C) STRANDEDNESS: single
　　　　(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Gln Ala Leu Gly Gly Lys Asn Pro Asp Phe His Arg Gln Asp Leu
1   5   10   15

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Gly Arg Tyr Pro Glu
1   5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Phe Asp Phe Asp Leu Leu Asp Pro Thr Lys
1   5   10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ile Ile Pro Glu Glu Leu Val Pro Phe Thr Pro Ile Gly Lys
1   5   10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Other
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AARAAYCCVG AYTTY   15

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Other

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(ix) FEATURE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTNCCDATNG TRAA   14

        (2) INFORMATION FOR SEQ ID NO:12:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 22 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: Other

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGGAATCCTC CGACCCTACG GA   22

        (2) INFORMATION FOR SEQ ID NO:13:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 27 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: Other

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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1

SEQUENCE LISTING

<110> THE GOVERNMENT OF THE UNITED STATES OF AMERICA, AS REPRESENTED BY
THE
DEPARTMENT OF HEALTH AND HUMAN SERVICES CENTERS FOR DISEASE
CONTROL AND
PREVENTION
ZANCOPE-OLIVEIRA, ROSALY M.
LOTT, TIMOTHY J.
MAYER, LEONARD W.
REISS, ERROL
DEEPE, JR., GEORGE S.

<120> NUCLEIC ACIDS OF THE M ANTIGEN GENE OF
HISTOPLASMA CAPSULATUM, ISOLATED AND RECOMBINANTLY-PRODUCED
ANTIGENS, VACCINES AND ANTIBODIES, METHODS AND KITS FOR
DETECTING HISTOPLASMOSIS

<130> 65798 / US

<140> NYA
<141> 1999-04-27

<150> U.S. 60/083,676
<151> 1998-04-30

<150> PCT/US99/09151
<151> 1999-04-27

<160> 13

<170> FastSEQ for Windows Version 3.0

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ctctcacatt caatctatat ttgatccttg tcctttgtag ctgtttaaat ataagccaag     3420
agagacaaat aatgatagat taacaaataa ttgcacaccc aataggcctt ccctcacgat     3480
atcagatatt atctatcatg ttgtaatgat acctcaaaaa tgccacaagc ttgcctgata     3540
ttgaatattt atatgctgta aatgtaggga agagcgtacc atccaaataa ccagaaaaac     3600
atgtttagc ttaaaatctc actaaggtcg gtcgtgtcta tttgaaatgg ctgcggcaag      3660
ctgactatct gataaaaatg tctgtatttc cgcttcacga cgcatgttat gactttcgaa     3720
tatagataaa acctgaacga tttagcccct gttgggggaa ataggggtta ggggggcgag     3780
```

```
ctacatatca ttcccatatg accaaaaact aaaatagata tatatatata tatatatata      3840
tacaacacct tcaaaaagga tcc                                              3863
```

<210> 2
<211> 705
<212> PRT
<213> Histoplasma capsulatum

<400> 2

```
Met Pro Ser Gly Gln Lys Gly Pro Leu Asp Arg Arg His Asp Thr Leu
1               5                   10                  15
Ser Asp Pro Thr Asp Gln Phe Leu Ser Lys Phe Tyr Ile Asp Asp Glu
            20                  25                  30
Gln Ser Val Leu Thr Thr Asp Val Gly Gly Pro Ile Glu Asp Gln His
            35                  40                  45
Ser Leu Lys Ala Gly Asn Arg Gly Pro Thr Leu Leu Glu Asp Phe Ile
        50                  55                  60
Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg Val Pro Glu Arg
65                  70                  75                  80
Ala Val His Ala Arg Gly Ala Gly Ala His Gly Val Phe Thr Ser Tyr
                85                  90                  95
Asn Asn Trp Ser Asn Ile Thr Ala Ala Ser Phe Leu Asn Ala Ala Gly
            100                 105                 110
Lys Gln Thr Pro Val Phe Val Arg Phe Ser Thr Val Ala Gly Ser Arg
            115                 120                 125
Gly Ser Val Asp Ser Ala Arg Asp Ile His Gly Phe Ala Thr Arg Leu
        130                 135                 140
Tyr Thr Asp Glu Gly Asn Phe Asp Ile Val Gly Asn Asn Val Pro Val
145                 150                 155                 160
Phe Phe Ile Gln Asp Ala Ile Gln Phe Pro Asp Leu Ile His Ala Val
                165                 170                 175
Lys Pro Gln Pro Asp Ser Glu Ile Pro Gln Ala Ala Thr Ala His Asp
            180                 185                 190
Thr Ala Trp Asp Phe Leu Ser Gln Gln Pro Ser Ser Leu His Ala Leu
            195                 200                 205
Phe Trp Ala Met Ser Gly His Gly Ile Pro Arg Ser Met Arg His Val
    210                 215                 220
Asp Gly Trp Gly Val His Thr Phe Arg Leu Val Thr Asp Glu Gly Asn
225                 230                 235                 240
Ser Thr Leu Val Lys Phe Arg Trp Lys Thr Leu Gln Gly Arg Ala Gly
                245                 250                 255
Leu Val Trp Glu Glu Ala Gln Ala Leu Gly Gly Lys Asn Pro Asp Phe
                260                 265                 270
His Arg Gln Asp Leu Trp Asp Ala Ile Glu Ser Gly Arg Tyr Pro Glu
            275                 280                 285
Trp Glu Leu Gly Phe Gln Leu Val Asn Glu Ala Asp Gln Ser Lys Phe
    290                 295                 300
Asp Phe Asp Leu Leu Asp Pro Thr Lys Ile Ile Pro Glu Glu Leu Val
305                 310                 315                 320
Pro Phe Thr Pro Ile Gly Lys Met Val Leu Asn Arg Asn Pro Lys Ser
                325                 330                 335
Tyr Phe Ala Glu Thr Glu Gln Ile Met Phe Gln Pro Gly His Val Val
```

```
              340                      345                     350
Arg Gly Ile Asp Phe Thr Asp Asp Pro Leu Leu Gln Gly Arg Leu Tyr
         355                      360                     365
Ser Tyr Leu Asp Thr Gln Leu Asn Arg His Gly Gly Pro Asn Phe Glu
         370                      375                     380
Gln Leu Pro Ile Asn Arg Pro Arg Ile Pro Phe His Asn Asn Asn Arg
385                      390                      395                     400
Asp Gly Ala Gly Gln Met Phe Ile Pro Leu Asn Thr Ala Ala Tyr Thr
              405                      410                     415
Pro Asn Ser Met Ser Asn Gly Phe Pro Gln Gln Ala Asn Arg Thr His
              420                      425                     430
Asn Arg Gly Phe Phe Thr Ala Pro Gly Arg Met Val Asn Gly Pro Leu
         435                      440                     445
Val Arg Glu Leu Ser Pro Ser Phe Asn Asp Val Trp Ser Gln Pro Arg
450                      455                      460
Leu Phe Tyr Asn Ser Leu Thr Val Phe Glu Lys Gln Phe Leu Val Asn
465                      470                      475                     480
Ala Met Arg Phe Glu Asn Ser His Val Arg Ser Glu Thr Val Arg Lys
              485                      490                     495
Asn Val Ile Ile Gln Leu Asn Arg Val Asp Asn Asp Leu Ala Arg Arg
              500                      505                     510
Val Ala Leu Ala Ile Gly Val Glu Pro Pro Ser Pro Asp Pro Thr Phe
         515                      520                     525
Tyr His Asn Lys Ala Thr Val Pro Ile Gly Thr Phe Gly Thr Asn Leu
         530                      535                     540
Leu Arg Leu Asp Gly Leu Lys Ile Ala Leu Leu Thr Arg Asp Asp Gly
545                      550                      555                     560
Ser Phe Thr Ile Ala Glu Gln Leu Arg Ala Ala Phe Asn Ser Ala Asn
              565                      570                     575
Asn Lys Val Asp Ile Val Leu Val Gly Ser Ser Leu Asp Pro Gln Arg
              580                      585                     590
Gly Val Asn Met Thr Tyr Ser Gly Ala Asp Gly Ser Ile Phe Asp Ala
         595                      600                     605
Val Ile Val Val Gly Gly Leu Leu Thr Ser Ala Ser Thr Gln Tyr Pro
610                      615                      620
Arg Gly Arg Pro Leu Arg Ile Ile Thr Asp Ala Tyr Ala Tyr Gly Lys
625                      630                      635                     640
Pro Val Gly Ala Val Gly Asp Gly Ser Asn Glu Ala Leu Arg Asp Val
              645                      650                     655
Leu Met Ala Ala Gly Gly Asp Ala Ser Asn Gly Leu Asp Gln Pro Gly
              660                      665                     670
Val Tyr Ile Ser Asn Asp Val Ser Glu Ala Tyr Val Arg Ser Val Leu
         675                      680                     685
Asp Gly Leu Thr Ala Tyr Arg Phe Leu Asn Arg Phe Pro Leu Asp Arg
         690                      695                     700
Ser
705
```

          <210> 3
          <211> 8
          <212> PRT
          <213> Histoplasma capsulatum

```
<400> 3
Ser Asp Pro Thr Asp Gln Phe Leu
 1               5
```

```
<210> 4
<211> 15
<212> PRT
<213> Histoplasma capsulatum
```

```
<400> 4
Asp Phe Ile Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg
 1               5                   10                  15
```

```
<210> 5
<211> 9
<212> PRT
<213> Histoplasma capsulatum
```

```
<400> 5
Thr Leu Gln Gly Arg Ala Gly Leu Val
 1               5
```

```
<210> 6
<211> 16
<212> PRT
<213> Histoplasma capsulatum
```

```
<400> 6
Ala Gln Ala Leu Gly Gly Lys Asn Pro Asp Phe His Arg Gln Asp Leu
 1               5                   10                  15
```

```
<210> 7
<211> 6
<212> PRT
<213> Histoplasma capsulatum
```

```
<400> 7
Ser Gly Arg Tyr Pro Glu
 1               5
```

```
<210> 8
<211> 10
<212> PRT
<213> Histoplasma capsulatum
```

```
<400> 8
Phe Asp Phe Asp Leu Leu Asp Pro Thr Lys
 1               5                   10
```

```
<210> 9
<211> 14
<212> PRT
```

<213> Histoplasma capsulatum

<400> 9
Ile Ile Pro Glu Glu Leu Val Pro Phe Thr Pro Ile Gly Lys
1   5   10

<210> 10
<211> 15
<212> DNA
<213> Unknown

<220>
<223> Primer

<400> 10
aaraayccvg aytty   15

<210> 11
<211> 14
<212> DNA
<213> Unknown

<220>
<223> primer; n= a, t, g or c

<400> 11
ttnccdatng traa   14

<210> 12
<211> 22
<212> DNA
<213> Unknown

<220>
<223> Primer

<400> 12
cggaatcctc cgaccctacg ga   22

<210> 13
<211> 27
<212> DNA
<213> Unknown

<220>
<223> Primer

<400> 13
accaagcttc tatccaacgg gaaccga   27